

AMENDMENTS TO THE SPECIFICATION

IN THE SPECIFICATION

Amend the paragraph on page 15, line 1 as follows:

According to the process of the herein invention a sequence of four internal peptides and of the N-terminal were determined. The N-terminal portion contains 46 amino acids residues (DVVIDGACPDMDKAVSKFDMNAYQGTWYEIKKFPVANEANGDCGSVE) (SEQ ID NO: 1) and the internal peptide fragments are:

- Fragment I (KSHVYTVPFGA) (SEQ ID NO: 2);
- Fragment II (KSNQHRVNIWILSRTK) (SEQ ID NO: 3)
- Fragment III (VRAGHVE) (SEQ ID NO: 4)
- Fragment IV (FDQSKFVETDFSEKACFF) (SEQ ID NO: 5).

The sequence obtained corresponds to about 15% of the whole protein and molecular mass of 69KDa.

Amend the paragraph beginning on page 15, line 28 as follows:

This invention is also related to the N-terminal sequence and the Sequence of internal fragments of the prothrombin activator fraction characterized by containing the N-terminal portion with 46 amino acids residues (DVVIDGACPDMDKAVSKFDMNAYQGTWYEIKKFPVANEANGDCGSVE) (SEQ ID NO: 1). The fragments of internal peptides are Fragment I (KSHVYTVPFGA) (SEQ ID

NO: 2); Fragment II (KSNQHRVNIWILSRTK) (SEQ ID NO: 3); Fragment III (VRAGHVE) (SEQ ID NO: 4) and Fragment IV (FDQSKFVETDFSEKACFF) (SEQ ID NO: 5) resulting in a sequence that corresponds to about 15% of the whole protein and molecular mass of 69 Kda.

Amend the paragraph beginning on page 28, line 25 as follows:

The N-terminal portion with 46 residues of amino acids (DVVIDGACPDMAKAVSKFDMNAYQGTWYEIKKFPVANEANGDCGSVE) (SEQ ID NO: 1) was obtained from purified Lopap, as well as the sequence of some internal peptides fragments called Fragments I: KSHVYTVPFGA(SEQ ID NO: 2). Fragment II: KSNQHRVNIWILSRTK(SEQ ID NO: 3) Fragment III: VRAGHVE (SEQ ID NO: 4) and Fragment IV: FDQSKFVETDFSEKACFF(SEQ ID NO: 5). The sequence that was obtained corresponded to about 15% of the whole protein considering 69 kDa its molecular mass.

Amend the paragraph beginning on page 30, line 21 as follows:

The kinetic parameters determined for Lopap using the quenched fluorogenic substrate Abz-QTFFNPRTFGSQ-EDDnp (SEQ ID NO: 6), based on the prothrombin sequence were $K_{\text{mapp}} 4,5 \mu\text{M}$; $K_{\text{cat}} 5,32 \text{ sec}^{-1}$; $K_{\text{cat}}/K_{\text{mapp}} 1,2 \times 10^6 \text{ M}^{-1} \text{ sec}^{-1}$. This indicates good relation and high catalytic efficiency for the studied enzyme, being these parameters obtained in accordance with what was described by Chagas et al. Lopap has shown activity on the Abz-YQTFFNPRTFGSQ-EDDnp (SEQ

ID NO: 7) substrate (deduced from prothrombin molecule) which was hydrolyzed in two sites Phe-Phe (10%) and Arg-Thr (90%) (Fig. 3)

Amend the paragraph beginning on page 46, line 3 as follows:

- A) Abz-YQTFFNPRTFGSQ-EDDnp (SEQ ID NO: 7) was incubated with Lopap in 50mM Tris-HCl buffer, pH 8,0 at 37°C for 3 h. The incubation mixture was analyzed through chromatography in HPLC as described in Manner and Process of making and using it.
- B) The Michaelis-Menten profile obtained with 0.8 - 8.0 μ M of fluorescent substrate hydrolysed by 73.3 pM of Lopap.

IN THE SEQUENCE LISTING

Please replace the Sequence Listing of record with the Substitute Sequence Listing enclosed herewith.